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<p>2/52</p> <p><i>Fig.1(i)</i></p>	<p>3/52</p> <p><i>Fig.1(ii)</i></p>
<p>4/52</p> <p><i>Fig.1(iii)</i></p>	<p>5/52</p> <p><i>Fig.1(iv)</i></p>

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1	TCGGCCTCC GAAACC ATG AAC TTT CTG	Met Asn Phe Leu
		1
50	CTT GCC TTG CTG CTC TAC CTC CAC	Leu Ala Leu Leu Leu Tyr Leu His
		15
98	CCC ATG GCA GAA GGA GGA GGG CAG	Pro Met Ala Glu Gly Gly Gly Gln
		30 35
146	ATG GAT GTC TAT CAG CGC AGC TAC	Met Asp Val Tyr Gln Arg Ser Tyr
		45 50
194	GAC ATC TTC CAG GAG TAC CCT GAT	Asp Ile Phe Gln Glu Tyr Pro Asp
		60 65
242	TCC TGT GTG CCC CTG ATG CGA TGC	Ser Cys Val Pro Leu Met Arg Cys
		80
290	CTC GAG TGT GTG CCC ACT GAG GAG	Leu Glu Cys Val Pro Thr Glu Glu
		95
338	CGG ATC AAA CCT CAC CAA GGC CAG	Arg Ily Lys Pro His Gln Gly Gln
		110 115

Fig.1(i)

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CTG TCT TGG GTG CAT TGG AGC Leu Ser Trp Val His Trp Ser 5 10	49
CAT GCC AAG TGG TCC CAG GCT GCA His Ala Lys Trp Ser Gln Ala Ala 20 25	97
AAT CAT CAC GAA GTG GTG AAG TTC Asn His His Glu Val Val Lys Phe 40	145
TGC CAT CCA ATC GAG ACC CTG GTG Cys His Pro Ile Glu Thr Leu Val 55	193
GAG ATC GAG TAC ATC TTC AAG CCA Glu Ile Glu Tyr Ile Phe Lys Pro 70 75	241
GGG GGC TGC TGC AAT GAC GAG GGC Gly Gly Cys Cys Asn Asp Glu Gly 85 90	289
TCC AAC ATC ACC ATG CAG ATT ATG Ser Asn Ile Thr Met Gln Ile Met 100 105	337
CAC ATA GGA GAG ATG AGC TTC CTA His Ile Gly Glu Met Ser Phe Leu 120	385

Fig.1(iii)

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386	CAG CAC AAC AAA TGT GAA TGC AGA
	Gln His Asn Lys Cys Glu Cys Arg
	125 130
434	GAA AAT CCC TGT GGG CCT TGC TCA
	Glu Asn Pro Cys Gly Pro Cys Ser
	140 145
482	CAA GAT CCG CAG ACG TGT AAA TGT
	Gln Asp Pro Gln Thr Cys Lys Cys
	160
530	TGC AAG GCG AGG CAG CTT GAG TTA
	Cys Lys Ala Arg Gln Leu Glu Leu
	175
578	AAG CCG AGG CGG TGAGCCGGGC AGGAG
	Lys Pro Arg Arg
	190
630	GAACCAGATC TCTCACCAGG

Fig.1(iii)

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CCA AAG AAA GAT AGA GCA AGA CAA	433
Pro Lys Lys Asp Arg Ala Arg Gln	
135	
GAG CGG AGA AAG CAT TTG TTT GTA	481
Glu Arg Arg Lys His Leu Phe Val	
150 155	
TCC TGC AAA AAC ACA GAC TCG CGT	529
Ser Cys Lys Asn Thr Asp Ser Arg	
165 170	
AAC GAA CGT ACT TGC AGA TGT GAC	577
Asn Glu Arg Thr Cys Arg Cys Asp	
180 185	
GAAGG AGCCTCCCTC AGCGTTTCGG	629

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Fig.1(iv)

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<p>7/52</p> <p>Fig.2(i)</p>	<p>8/52</p> <p>Fig.2(ii)</p>
<p>9/52</p> <p>Fig 2(iii)</p>	<p>10/52</p> <p>Fig 2(iv)</p>
<p>11/52</p> <p>Fig 2(v)</p>	<p>12/52</p> <p>Fig 2(vi)</p>

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1	CC ATG AGC CCT CTG CTC CGC CGC	
	Met Ser Pro Leu Leu Arg Arg	
	1 5	
48	CTG GCC CCC GCC CAG GCC CCT GTC	
	Leu Ala Pro Ala Gln Ala Pro Val	
	20	
96	CAG AGG AAA GTG GTG TCA TGG ATA	
	Gln Arg Lys Val Val Ser Trp Ile	
	35	
144	CAG CCC CGG GAG GTG GTG GTG CCC	
	Gln Pro Arg Glu Val Val Val Pro	
	50 55	
192	GTG GCC AAA CAG CTG GTG CCC AGC	
	Val Ala Lys Gln Leu Val Pro Ser	
	65 70	
240	GGC TGC TGC CCT GAC GAT GGC CTG	
	Gly Cys Cys Pro Asp Asp Gly Leu	
	80 85	
288	CAA GTC CGG ATG CAG ATC CTC ATG	
	Gln Val Arg Met Gln Ile Leu Met	
	100	
336	GGG GAG ATG TCC CTG GAA GAA CAC	
	Gly Glu Met Ser Leu Glu Glu His	
	115	

Fig.2(i)

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CTG	CTG	CTC	GCC	GCA	CTC	CTG	CAG	47
Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	
		10					15	
TCC	CAG	CCT	GAT	GCC	CCT	GGC	CAC	95
Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	
	25					30		
GAT	GTG	TAT	ACT	CGC	GCT	ACC	TGC	143
Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	
40					45			
TTG	ACT	GTG	GAG	CTC	ATG	GGC	ACC	191
Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	
			60					
TGC	GTG	ACT	GTG	CAG	CGC	TGT	GGT	239
Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
			75					
GAG	TGT	GTG	CCC	ACT	GGG	CAG	CAC	287
Glu	Cys	Val	Pro	Thr	Gly	Gln	His	
		90					95	
ATC	CGG	TAC	CCG	AGC	AGT	CAG	CTG	335
Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
	105					110		
AGC	CAG	TGT	GAA	TGC	AGA	CCT	AAA	383
Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
120					125			

Fig. 2(ii)

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384	AAA	AAG	GAC	AGT	GCT	GTG	AAG	CCA
	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro
			130					135
432	CGT	CCC	CAG	CCC	CGT	TCT	GTT	CCG
	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro
		145					150	
480	CCC	TCC	CCA	GCT	GAC	ATC	ACC	CAT
	Pro	Ser	Pro	Ala	Asp	Ile	Thr	His
	160					165		
528	GCC	CAC	GCT	GCA	CCC	AGC	ACC	ACC
	Ala	His	Ala	Ala	Pro	Ser	Thr	Thr
				180				
576	GCT	GCC	GCT	GCC	GAC	GCC	GCA	GCT
	Ala	Ala	Ala	Ala	Asp	Ala	Ala	Ala
				195				

Fig. 2(iii)

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GAC	AGG	GCT	GCC	ACT	CCC	CAC	CAC	431
Asp	Arg	Ala	Ala	Thr	Pro	His	His	
				140				
GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	479
Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	
			155					
CCC	ACT	CCA	GCC	CCA	GGC	CCC	TCT	527
Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	
		170					175	
AGC	GCC	CTG	ACC	CCC	GGA	CCT	GCC	575
Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	
	185					190		
TCC	TCC	GTT	GCC	AAG	GGC	GGG	GCT	T 624
Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
200					205			

Fig.2(iv)

11/52

625	AGAGCTCAAC	CCAGACACCT	GCAGGTGCCG
685	GACTCAGCAG	GGTGACTTGC	CTCAGAGGCT
745	GGTAAAAAAC	AGCCAAGCCC	CCAAGACCTC
805	GCCTCTCAGA	GGGCTCTTCT	GCCATCCCTT
865	GAGTTGGAAG	AGGAGACTGG	GAGGCAGCAA
825	GGAGTACTGT	CTCAGTTTCT	AACCACTCTG
985	CTCCCCTCAC	TAAGAAGACC	CAAACCTCTG
1045	CTGTGACCCC	CAACCCTGAT	AAAAGAGATG

Fig.2(v)

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GAAGCTGCGA AGGTGACACA TGGCTTTTCA	684
ATATCCCAGT GGGGGAACAA AGGGGAGCCT	744
AGCCCAGGCA GAAGCTGCTC TAGGACCTGG	804
GTCTCCCTGA GGCCATCATC AAACAGGACA	864
GAGGGGTCAC ATACCAGCTC AGGGGAGAAT	924
TGCAAGTAAG CATCTTACAA CTGGCTCTTC	984
CATAATGGGA TTTGGGCTTT GGTACAAGAA	1044
GAAGGAAAAA AAAAAAAAAA	1094

Fig.2(vi)

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Fig.3(i)	Fig.3(ii)

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>VEGF_HUMAN VEGF_HUMAN VASCULAR ENDOTHELIAL
(VASCULAR 215 AA.
LENGTH = 215

SCORE = 181 (92.4 BITS), EXPECT = $6.4e-20$,
IDENTITIES = 33/75 (44%), POSITIVES = 48/75

QUERY: 31 HQRKVVSVIDVYTRATCQPREVVVPLTVEL
+++ VV +DVY R+ C+P E +V + E

SBJCT: 36 NHHEVVKFMDVYQRSYCHPIETLVDIFQEY

QUERY: 91 PTGQHQVRMQILMIR 105
PT + + MQI+ I+

SBJCT: 96 PTEESNITMQIMRIK 110

SCORE = 76 (38.8 BITS), EXPECT = 0.0011,
IDENTITIES = 12/19 (63%), POSITIVES = 16/19

QUERY: 110 QLGEMSLEEHSQCECRPKK 128
++GEMS +H+ CECRPKK

SBJCT: 116 HIGEMSFLQHNKCECRPKK 134

SCORE = 72 (36.8 BITS), EXPECT = 0.0046,
IDENTITIES = 14/21 (66%), POSITIVES = 15/21

QUERY: 202 RCQGRGLELNPDTTCRCRKLRR 222
RC +R LELN TCRC K RR

SBJCT: 195 RCKARQLELNERTCRCDKPRR 215

SCORE = 46 (23.5 BITS), EXPECT = 47.,
IDENTITIES = 6/10 (60%), POSITIVES = 9/10

QUERY: 187 DPRTTCRCRCR 196
DP+TC+C C+

SBJCT: 181 DPQTCKCSCK 190

Fig.3(i)

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GROWTH FACTOR PRECURSOR (VEGF)

$P = 6.4e-20$
(64%)

MGTVAKQLVPSCVTVQRCGGCCPDDGLECV 90
+ PSCV + RCGGCC D+GLECV
PDEIEYIFKPSCVPLMRCGGCCNDEGLECV 95

POISSON $P(2) = 9.1e-12$
(84%)

POISSON $P(3) = 3.6e-18$
(71%)

POISSON $P(4) = 7.3e-10$
(90%)

Fig.3(i)

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<p>17/52</p> <p>Fig.4(i)</p>	<p>18/52</p> <p>Fig.4(ii)</p>
<p>19/52</p> <p>Fig.4(iii)</p>	<p>20/52</p> <p>Fig.4(iv)</p>

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Gap Weight:3.00	Average Match:1.000
Length Weight:0.100	Average Mismatch:-0.900
Quality:100.9	Length:739
Ratio:0.175	Gaps:30
Percent	Percent
Similarity:69.703	Identity:69.703

28	ATGAGCCCTCTGCTCCGCCGCCTGC
17	ATGAAC TTTCTGCT.....GTCT..
68	TGCAGCTGGCCCCCGCCCAGGCCCC
57	TGCTGCTCTACCTCCACCATGCCAA
118	CACCAGAGGA.....
106	AGAAGGAGGAGGGCAGAATCATCAC
140	GTGTATACTCGC.GCTACCTGCCAG
152	GTCTATCAGCGCAGCTA.CTGCCAT
194	T....GA.....CTGTGGAGCTCAT
201	TCCAGGAGTACCCTGATGAGATCGA
235	CCCAGCTGCGTGACTGTGCAGCGCT
239	CCATCCTGTGTGCCCCCTGATGCGAT
285	CCTGGAGTGTGTGCCCCACTGGGCAG
289	CCTGGAGTGTGTGCCCCACTGAGGAG

Fig.4(i)

18/52

TGCTCGCCGCACT.....CC	67
...TGGGTGCATTGGAGCCTTGCCT	56
TGTCTCCCAGCCTGATGCCCCTGGC	117
GTGGTCCCAGGCTGCA.CCCATGGC	105
.AAGTGGTG....TCATGGATAGAT	147
GAAGTGGTGAAGTTCATG....GAT	151
CCCCGGGAG...GTGGTGGTGCCCT	193
CCAATCGAGACCCTGGTGGACATCT	200
GGGCACCGTGGCCAAACAGCTGGTG	234
GTACATCTT...CAA.....G	238
GTGGTGGCTGCTGCCCTGACGATGG	284
GCGGGGGCTGCTGCAATGACGAGGG	288
CACCAAGTCCGGATGCAGAT.....	329
TCCAACATCACCATGCAGATTATGC	338

Fig.4(ii)

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```

330      .....CCTCATGATCCGGTACC
          |||||
339      GGATCAAACCTCA.....C
          |
369      GTCCCTGGAAGAACACAGCCAGTGT
          | | | | | | | | | |
376      GAGCTTCCTACAGCACAAATGT
          |
419      GTGCTGTGAAGCCAGACAGGGCTGC
          | | | | | | |
423      G.....AGCAAGACAAG.....
          |
469      CGTTCTGTTCCGGGCTGGGACTCTG
          | | | | | | |
443      ...TGTGGGCCTTGCTCAGA.....
          |
519      CATCACCCATCCCCTCCAGCCCCA
          |
468      .....
          |
569      GC.....ACCACCAGCGCCC
          || | | |
469      GCATTTGTTTGTACAA.....
          |
609      TGCCGACGCCGCAGCTTCCTCCGTT
          || | | | | | |
509      TG.CAAAACACAGACTC..GCGTT
          |
657      AACCCAGACACCTGCAGGTGCCGGA
          ||| |
554      AACGAACGTACTTGCAGATGTGACA

```

Fig. 4(iii)

20/52

CGAGCAGTCAGC...TGGGGGAGAT	368
CAAG..GCCAGCACATAGGAGAGAT	375
GAATGCAGACCTAAAAAAAGGACA	418
GAATGCAGACC...AAAGAAAGATA	422
CACTCCCCACCACCGTCCCCAGCCC	468
.....AAAATCCC.....	442
CCCCCGGAGCACCCTCCCCAGCTGA	518
...GCGGAGAA.....	467
GGCCCCCTCTGCCCACGCTGCACCCA	568
.....A	468
TGACCCCCGGACCTGCCGCTGCCGC	608
.GATCCGCAGACGTGTAAATGTTCC	508
GCCAAGGGCGGGGC..TTAGAGCTC	656
GC..AAGGCGAGGCAGCTTGAGTTA	553
AGCTGCGAAGGTGA	695
AGCCGAGGCGGTGA	592

Fig.4(iv)

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<i>22/52</i> <i>Fig.5(i)</i>	<i>23/52</i> <i>Fig.5(ii)</i>	<i>24/52</i> <i>Fig.5(iii)</i>
<i>25/52</i> <i>Fig.5(iv)</i>	<i>26/52</i> <i>Fig.5(v)</i>	<i>27/52</i> <i>Fig.5(vi)</i>

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165SOMSQ.MSF.msf MSF:687

Type: D Tuesday, June 20, 1995

Check:3140

	1
VEGF165	ATGAACTTTCTGCTGTCTTGGGTG
SOM175	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6&7	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e4	ATGAGCCCTCTGCTCCGCCGCCTG
	81
VEGF165	CACCCATGGCAGAAGGAGGAGGGC
SOM175	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6&7	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e4	TGCCCCTGGCCACCAGAGGAAAGT
	161
VEGF165	CCAATCGAGACCCTGGTGGACATC
SOM175	GTGGTGGTGGCCCTTGACTG.TGGA
SOM175-e6	GTGGTGGTGGCCCTTGACTG.TGGA
SOM175-e6&7	GTGGTGGTGGCCCTTGACTG.TGGA
SOM175-e4	GTGGTGGTGGCCCTTGACTG.TGGA
	241
VEGF165	GATGCGATGCGGGGGCTGCTGCAA
SOM175	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6&7	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e4	GCAGCGCTGTGGTGGCTGCTGCCC

Fig.5(i)

23/52

CATTGGAGCCTTGCCTTGCTGCTCTACC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC

AGAATCATCACGAAGTGGTGAAGTTCAT
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC

TTCCAGGAGTACCCTGATGAGATCGAGT
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC

TGACGAGGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT

Fig. 5(ii)

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80
TCCACCATGCCAAGTGGTCCCAGGCTG.
CCGCCCAGGCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCTGTCTCCCAGCCTGA

160
GGATGTCTATCAGCGCAGCTACTGCCAT
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG

240
ACATCTTCAAGCCATCCTGTGTGCCCCT
TGGTGCCCAG.....CTGCGTGACTGT
TGGTGCCCAG.....CTGCGTGACTGT
TGGTGCCCAG.....CTGCGTGACTGT
TGGTGCCCAG.....CTGCGTGACTGT

320
GAGGAGTCCAACATCACCATGCAGATTA
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGA...

Fig.5(iii)

	321
VEGF165	TGCGGATCAAACCTCACCAAGGCC
SOM175	TCATGATCCGG...TACCCGAGCA
SOM175-e6	TCATGATCCGG...TACCCGAGCA
SOM175-e6&7	TCATGATCCGG...TACCCGAGCA
SOM175-e4
	401
VEGF165	AAGAAAGATAG.....AGCAA
SOM175	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6&7	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e4	AAAAAGGACAGTGCTGTGAAGCCA
	481
VEGF165AAGCA.....
SOM175	CTCTGCCCCCGGAGCACCCCTCCCC
SOM175-e6
SOM175-e6&7
SOM175-e4	CTCTGCCCCCGGAGCACCCCTCCCC
	561
VEGF165	A.....GATCCGCA
SOM175	GCACCACCAGCGCCCTGACCCCCG
SOM175-E6	GCACCACCAGCGCCCTGACCCCCG
SOM175-e6&7
SOM175-e4	GCACCACCAGCGCCCTGACCCCCG
	641
VEGF165	TTGAGTTAAACGAACGTACTTGCA
SOM175	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6&7
SOM175-e4	TAGAGCTCAACCCAGACACCTGCA

Fig.5(iv)

AGCACATAGGAGAGATGAGCTTCCTACA
 GTCAGCTGGGGGAGATGTCCCTGGAAGA
 GTCAGCTGGGGGAGATGTCCCTGGAAGA
 GTCAGCTGGGGGAGATGTCCCTGGAAGA

.....

GACAAGAA....AATCCCTGTGG.....
 GACAGGGCTGCCACTCCCCACCACCGTC
 GATAG.....
 GATAG.....
 GACAGGGCTGCCACTCCCCACCACCGTC

.....
 AGCTGACATCACCCATCCCCACTCCAGCC
CC

 AGCTGACATCACCCATCCCCACTCCAGCC

GACGTGTAAATGTTCTTGCAAAAAC.AC
 GACCTGCCGCTGCCGCTGCCGACGCCGC
 GACCTGCCGCTGCCGCTGCCGACGCCGC

 GACCTGCCGCTGCCGCTGCCGACGCCGC

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GATGTGACAAGCCGAGGCGGTGA
 GGTGCCGGAAGCTGCGAAGGTGA
 GGTGCCGGAAGCTGCGAAGGTGA
 .GTGCCGGAAGCTGCGAAGGTGA
 GGTGCCGGAAGCTGCGAAGGTGA

Fig.5(v)

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400

GCACAACAAATGTGAATGCAGACC...A
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
.....CCTAAA

480

.....GCCTTGCTCAGAGCGGAGA
CCCAGCCCCGTTCTGTTCCGGGCTGGGA
.....
.....
CCCAGCCCCGTTCTGTTCCGGGCTGGGA

560

.....TTTGTT.....TGTAC...A
CCAGGCCCCCTCTGCCCCACGCTGCACCCA
CCAGGCCCCCTCTGCCCCACGCTGCACCCA
.....
CCAGGCCCCCTCTGCCCCACGCTGCACCCA

640

AGACTCG..CGTTGCAAGGCGAGGCAGC
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
.....
AGCTTCCTCCGTTGCCAAGGGCGGGGCT

Fig.5(vi)

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<i>Fig 6(i)</i>	<i>29/52</i>	<i>Fig 6(ii)</i>	<i>30/52</i>
<i>Fig 6(iii)</i>	<i>31/52</i>		

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VEGF ₁₆₅	M	N	F	L	L	S	W	V	H	W	S	L	A	L	L	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P
SOM175 _{Short}	M	S	P	L	L	R	R	L	L	.	.	L	A	A	L	L	L	Q	L	A	P	A	Q	A	P
VEGF ₁₆₅	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N	
SOM175 _{Short}	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	G	C	C	P	
VEGF ₁₆₅	F	L	Q	H	N	K	C	E	C	R	P	K	K	D	R	A	
SOM175 _{Short}	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H	H	
VEGF ₁₆₅	C	K	C	S	C	K	N	T	D	S	R	C	K	A	R	Q	L	E	L	N	E	R	T	C	R	C	D	K	
SOM175 _{Short}	H	A	A	P	S	T	T	S	A	L	T	P	G	P	A	A	A	A	A	D	A	A	S	S	V	A	K		
OR...																													
VEGF ₁₆₅	M	N	F	L	L	S	W	V	H	W	S	L	A	L	L	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P
SOM175 _{Long}	M	S	P	L	L	R	R	L	L	.	.	L	A	A	L	L	L	Q	L	A	P	A	Q	A	P
VEGF ₁₆₅	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N	
SOM175 _{Long}	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	G	C	C	P	
VEGF ₁₆₅	F	L	Q	H	N	K	C	E	C	R	P	K	K	D	R	A	
SOM175 _{Long}	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H	H	
VEGF ₁₆₅	G	P	C	S	E	R	R	K	H	L	F	V	Q	D	P	Q	T	C	K	C	S	C	K	N	T	D	S	.	
SOM175 _{Long}	P	R	C	T	Q	H	H	Q	R	.	.	P	D	P	R	T	C	R	C	R	C	R	R	R	S	F	L		

Fig 6(i)

M A E G G Q N H H E . V V K F M D V Y Q R S Y C H P I E T L V D 60
 V S Q P D A P G H Q R K V V S W I D V Y T R A T C C P P R E V V P 55
 D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
 D D G L E C V P T G Q H Q V R M Q I L M I R . Y P S S Q L G E M S 115
 R Q E N P C G P C S E R R K H L F . V Q D P Q T 170
 R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P S A 175
 P R R
 G G A 191
 207

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M A E G G Q N H H E . V V K F M D V Y Q R S Y C H P I E T L V D 60
 V S Q P D A P G H Q R K V V S W I D V Y T R A T C C P P R E V V P 55
 D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
 D D G L E C V P T G Q H Q V R M Q I L M I R . Y P S S Q L G E M S 115
 R Q E N P P A P G A P S P A D I T H P T P A P G P L C 170
 R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P L C 177
 R C K A R Q L E L N E R T C R C D K P R R 191
 R C Q G R G L E L N P D T C R C K L R R 222

Fig. 6 (iii)

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Areas of 100% homology are boxed and conserved residues thought to be involved in homodimerisation are underlined. The VEGF sequence depicted includes the 26 amino acid leader sequence (removal of which gives rise to mature VEGF₁₆₅) giving a total length of 191 amino acids.

Homology of SOM175 to VEGF₁₆₅ is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF).

ie. Cysteine-47
Proline-70, Cysteine-72, Valine-74
Arginine-77, Cysteine-78, Glycine-80, Cysteines-81 & 82
Cysteine-89, Proline-91
Cysteines 122 & 124

Fig.6(iii)

SPLICE VARIANTS OF SOM175

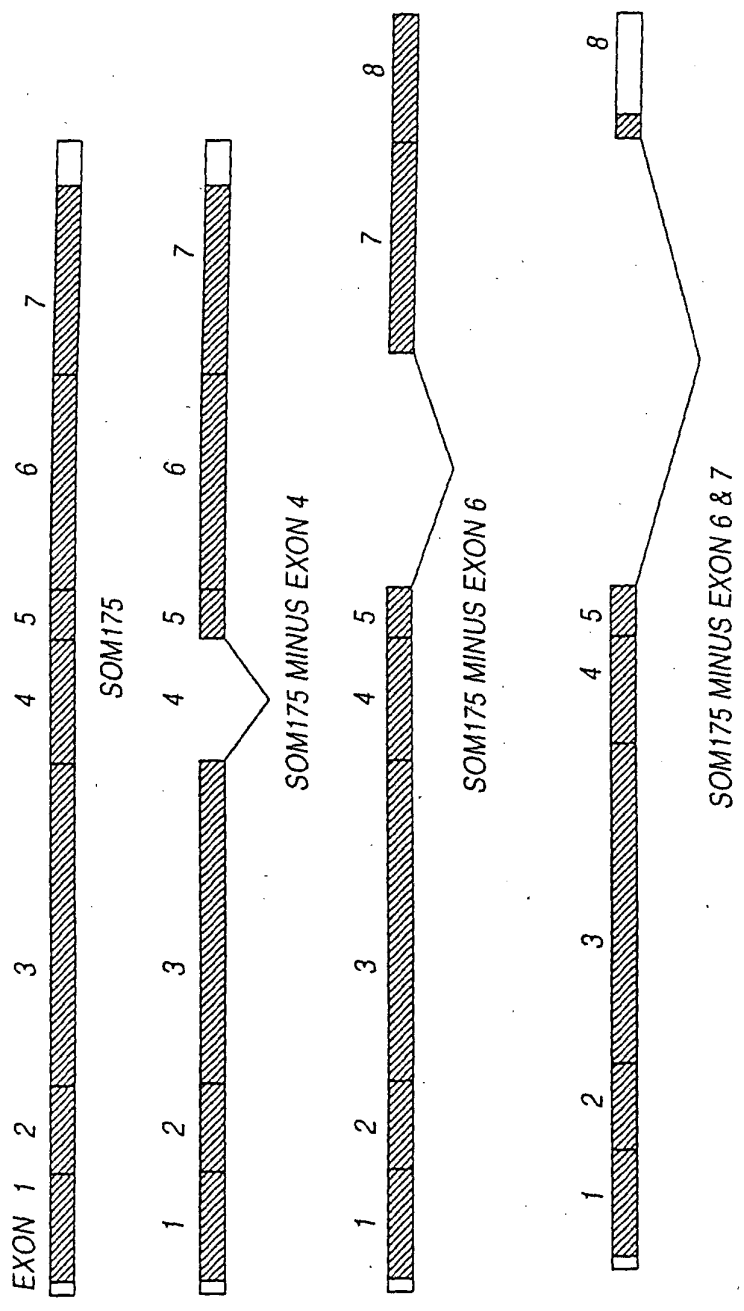


Fig. 7

GENOMIC STRUCTURE OF HUMAN SOM175

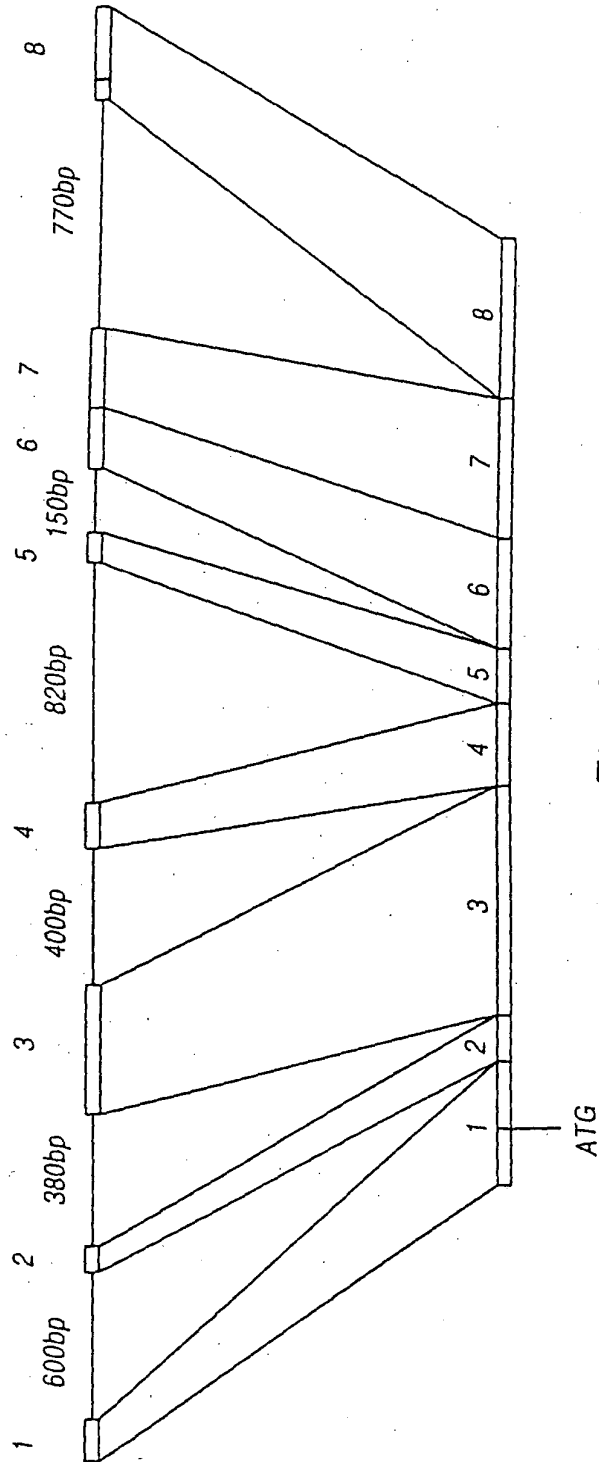


Fig. 8A

5'UTR... ATGAGG	*Exon 1 (60bp)	GGCCAG gtacgtgagg
tctccacacag GCCCCT	Exon 2 (43bp)	GGAAAG aatacttaca
tctgctccca TGGTGT	Exon 3 (187bp)	ATGCAG gtccgagatg
ctgaatacag ATCCTC	Exon 4 (73bp)	ATGCAG gtgtcaggca
acttttcaag ACCTAA	Exon 5 (34bp)	AGACAG gtgagtcttt
ctcctccgta GGCTGC	Exon 6 (101bp)	CTCCAG cccaggccc
cccactccag CCCCAG	Exon 7 (109bp)	ACCCAG acacctgtag
ccctgctcag GTGCCG	*Exon 8 (22bp)	AGGTGA ...3'UTR

Fig.8B

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36/52 <i>Fig. 9(i)</i>	37/52 <i>Fig. 9(ii)</i>
38/52 <i>Fig. 9(iii)</i>	39/52 <i>Fig. 9(iv)</i>

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-163 gcacgagctcaggccgctcgctgcggcgctg
-103 gggggccgcggaggagccgccccctgcgcc
-43 ggcggctctggctgacccccccccacaccg

16 CGTCGCCTGCTGCTTGTGCACTGCTGCAG
R R L L L V A L L Q

76 TTTGATGGCCCCAGTCACCAGAAGAAAGTG
F D G P S H Q K K V

136 ACATGCCAGCCCAGGGAGGTGGTGGTGCCT
T C Q P R E V V V P

196 AAACAAGTAGTGCCCAGCTGTGTGACTGTG
K Q L V P S C V T V

256 GGCCTGGAATGTGTGCCCAGTGGGCAACAC
G L E C V P T G Q H

316 TACCCGAGCAGTCAGCTGGGGGAGATGTCC
Y P S S Q L G E M S

376 CCTAAAAAAAAAGGAGAGTGCTGTGAGGCCA
P K K K E S A V R P

436 CAGCCCCGCTCTGTTCCGGGCTGGGACTCT
Q P R S V P G W D S

Fig.9(i)

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cgttgcgctgcctgcgcccagggctcgga	
ccgccccgggtccccgggtccgcgccatgg	
ccgggctagggccccgATGAGCCCCCTGCTG	
	M S P L L -17
CTGGCTCGCACCCAGGCCCTGTGTCCCAG	
L A R T Q A P V S Q	4
GTGCCATGGATAGACGTTTATGCACGTGCC	
V P W I D V Y A R A	24
CTGAGCATGGAATCATGGGCAATGTGGTC	
L S M E L M G N V V	44
CAGCGCTGTGGTGGCTGCTGCCCTGACGAT	
Q R C G G C C P D D	64
CAAGTCCGAATGCAGATCCTCATGATCCAG	
Q V R M Q I L M I Q	84
CTGGGAGAACACAGCCAATGTGAATGCAGA	
L G E H S Q C E C R	104
GACAGGGTTGCCATACCCACCCGTC	
D R V A I P H H R P	124
ACCCCGGGAGCACCTCCCCAGCTGACATC	
T P G A P S P A D I	144

Fig.9(iii)

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496	ATCCATCCC <u>ACTCCAG</u> CCCCAGGATCCTCT
	I H P T P A P G S S
	S P R I L
556	CTGACCCCCGGACCTGCCGTTGCCGCTGTA
	L T P G P A V A A V
	P D P R T C R C R C
616	GGGGCTTAGAGCTCAACCCAGACACCTGTA
	G A *
	R G L E L N P D T C
676	ctttccagactccacggggcccggtgcttt
736	agcacaggcgtaacctcctcagtctgggag
796	gagctctctcgccatcttttatctcccaga
856	atgtctcacctcaggggcccaggggtactctc
916	ttctggctggctgtctcccctcactatgaa
976	gggttctgttatgataactgtgacacacac
1036	gacactaaaaaaaaaaaaaaaaaaaaaaaaa

Fig.9(iii)

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GCCCGCCTTGCACCCAGCGCCGCCAACGCC	
A R L A P S A A N A	164
C P P C T Q R R Q R	130
GACGCCGCCGCTTCCTCCATTGCCAAGGGC	
D A A A S S I A K G	184
R R R R F L H C Q G	150
↓	
GGTGCCGGAAGCCGCGAAAGTGAcagctg	
R C R K P R K *	186
	167
tatggccctgcttcacagggagaagagtgg	
gtcactgccccaggacctggaccttttaga	
gctgccatctaacaattgtcaaggaacctc	
tcacttaaccaccctgggtcaagtgagcatc	
aaccccaaacttctaccaataacgggattt	
acacactcacactctgataaaagagatgga	
aaaaaaaaaaaa	

Fig.9(iv)

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Fig 10(i)	Fig 10(ii)

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A

hVRF167	-21	MSPLLRRLLLAALLQLAPAQAP	
mVRF167	-21	MSPLLRRLLLVALQLARTQAP	
hVRF167	30	EVVVPLTVELMGTVAKQLVPSC	
		:	
mVRF167	30	EVVVPLSMELMGNVVKQLVPSC	
hVRF167	80	ILMIRYPSSQLGEMSLEEHSQC	
		:	
mVRF167	80	ILMIQYPSSQLGEMSLGEHSQC	
hVRF167	130	RPDPRTCRCRCRRRSFLRCQGR	
		:	
mVRF167	130	RPDPRTCRCRCRRRRFLHCQGR	

B

hVRF186	116	RAATPHHRPQPRSVPGWDSAPG	
mVRF186	116	RVAIPHHRPQPRSVPGWDSTPG	
hVRF186	166	TPGPAAAAADAAASSVAKGGA*	
		:	
mVRF186	166	TPGPAVAVDAAASSIAKGGA*	

Fig.10(i)

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VSQPDAPGHQQRKVVSVIDVYTRATCQPR 29

||| |:|:|:| | | | | | | | |

VSQFDGPPSHQKKVVPWIDVYARATCQPR 29

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79

| | | | | | | | | | | | | | | | | | |

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79

ECRPKKKDSAVKPDSPRPLCPRCTQHHQ 129

| | | | | |:| |:| | | | | | | | | | |

ECRPKKKESAVRPDSPRILCPPCTQRRQ 129

GLELNPDTCRCKLRR* 167

| | | | | | | | | | | | | | |

GLELNPDTCRCKPRK* 167

APSPADITHPTPAPGPSAHAAPSTTSAL 165

| | | | | | | | | | | | | | | | |

APSPADIIHPTPAPGSSARLAPSAANAL 165

186

186

Fig.10(ii)

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44/52	45/52
Fig 11(i)	Fig 11(ii)

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mVRF167	-21	MSPLLRRLLVALLQL	:: :
mVEGF188	-26	MNFLLSVHWTALLLYLHH	
mVRF167	25	TCQPREVVVPLSMELMGNVV	: : ::
mVEGF188	24	YCRPIETLVDIFQEYPDEIE	
mVRF167	75	QVRMQILMIQYPSSQ.LGEM	: : :
mVEGF188	74	NITMQIMRIKPHQSQHIGEM	
mVRF167	119ILCPPC	:
mVEGF188	124	QKRKRKKS RFKSWSVHCEPC	
mVRF167	152	GLELNPDTCCRCRKPRK	:
mVEGF188	173	QLELNERTCRCDKPRR	

Fig.11(i)

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AR.TQAPVSQFDGPSHQKKVVPWIDVYARA	24
: : : : : : ::	
AKWSQAAPTT.EGEQKSHEVIKFMDVYQRS	23
KQLVPSCVTVQRCGGCCPDDGLECVPTGQH	74
: : : : : ::	
YIFKPSCVPLMRCAGCCNDEALECVPTSES	73
SLGEHSQCECRPKKKESAVRPDSPR.....	118
: :	
SFLQHSRCECRPKKDRTKPEKKSVRGKGKG	123
TQRRQR...PDPRTCRCRCRRRFLHCQGR	151
: : : : : :	
SERRKHLFVQDPQTCKCCKNTDS.RCKAR	172
	167
	188

Fig.11(ii)

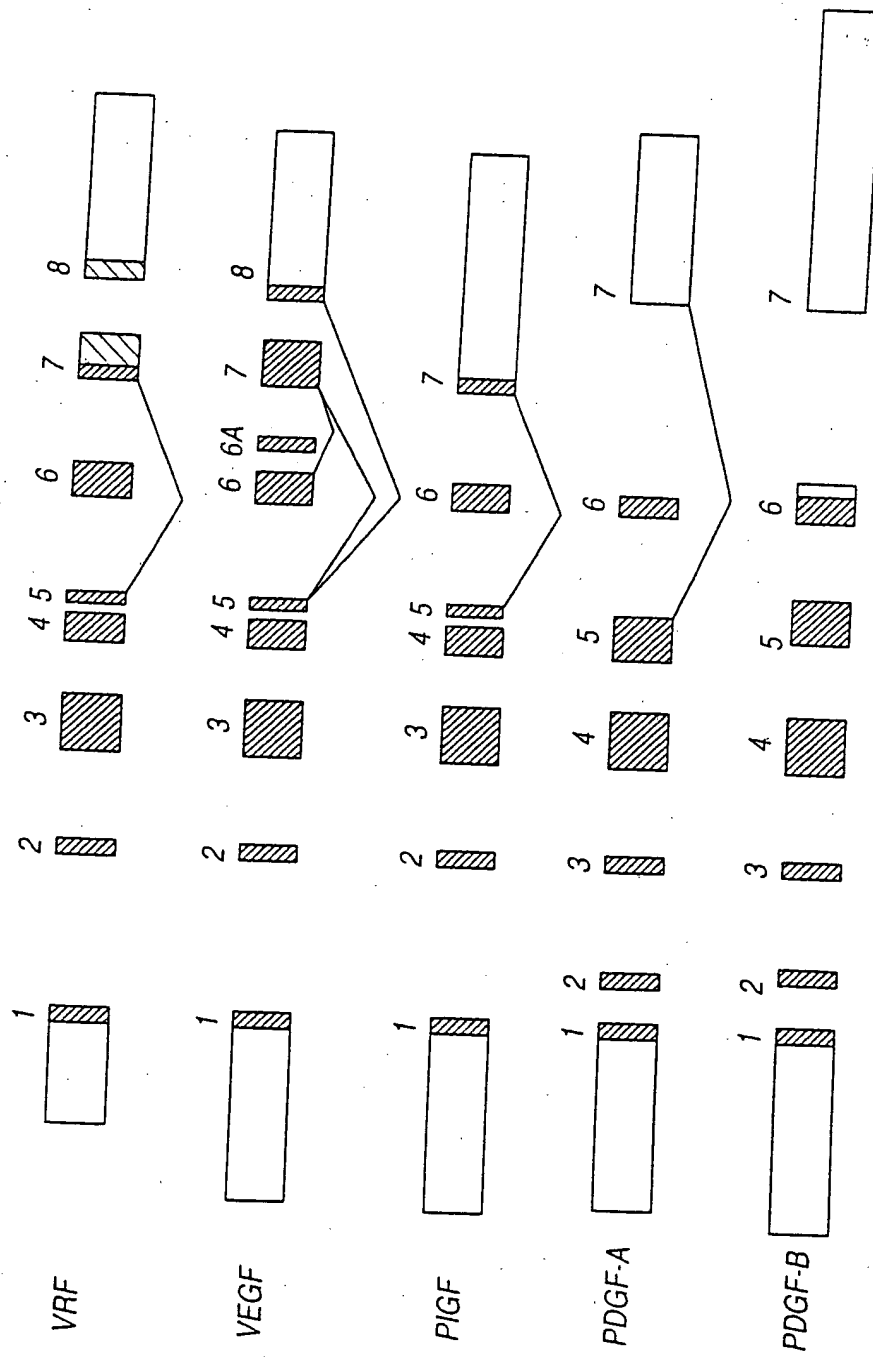


Fig.12

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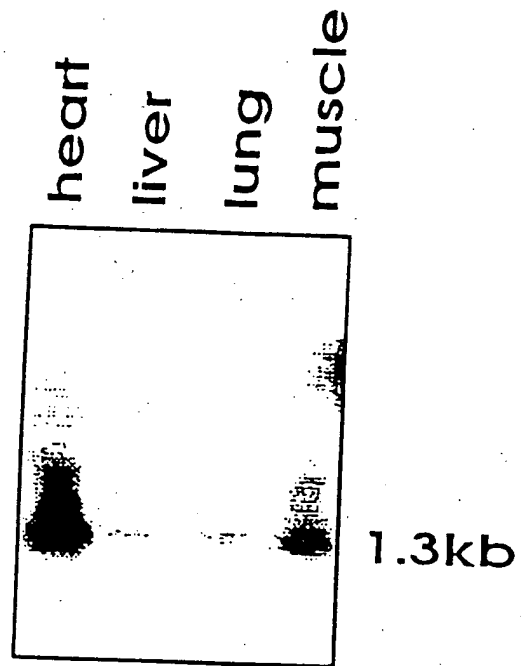


Fig.13

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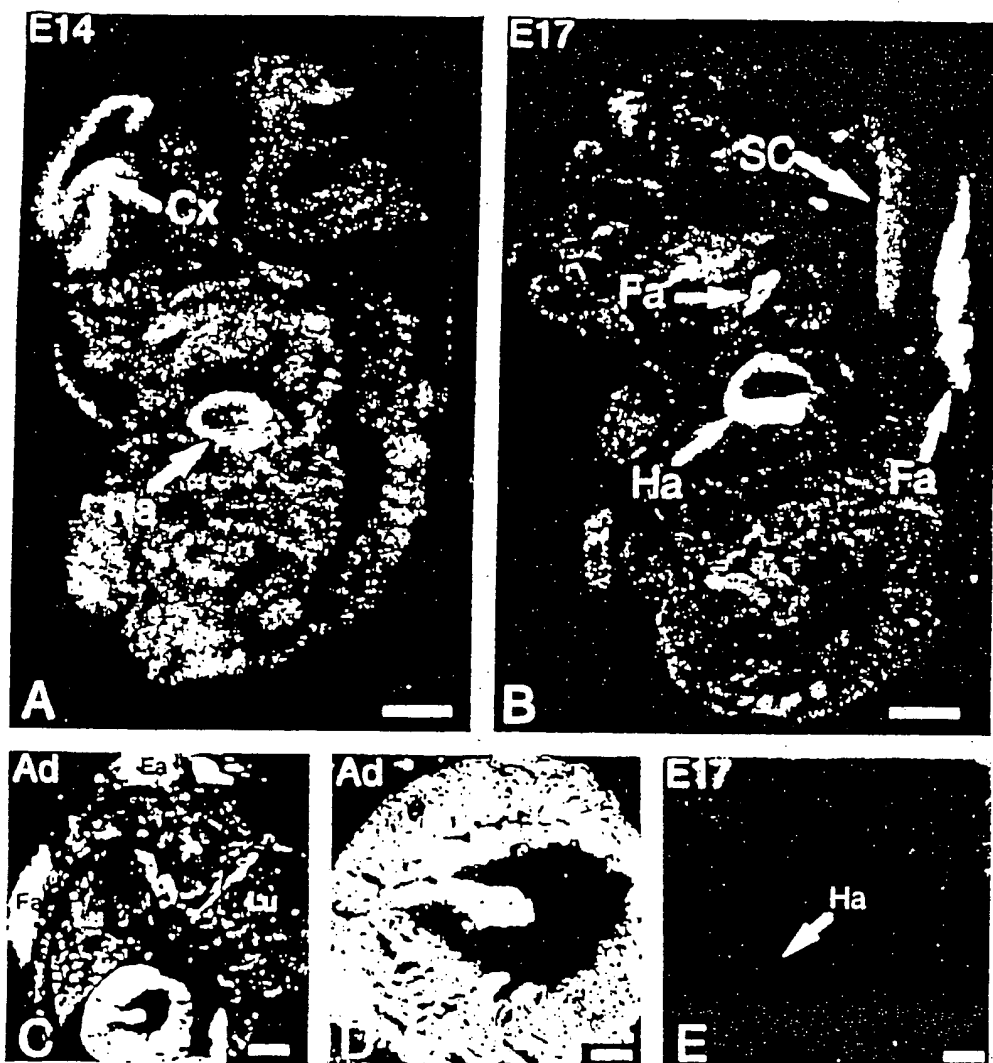


Fig.14

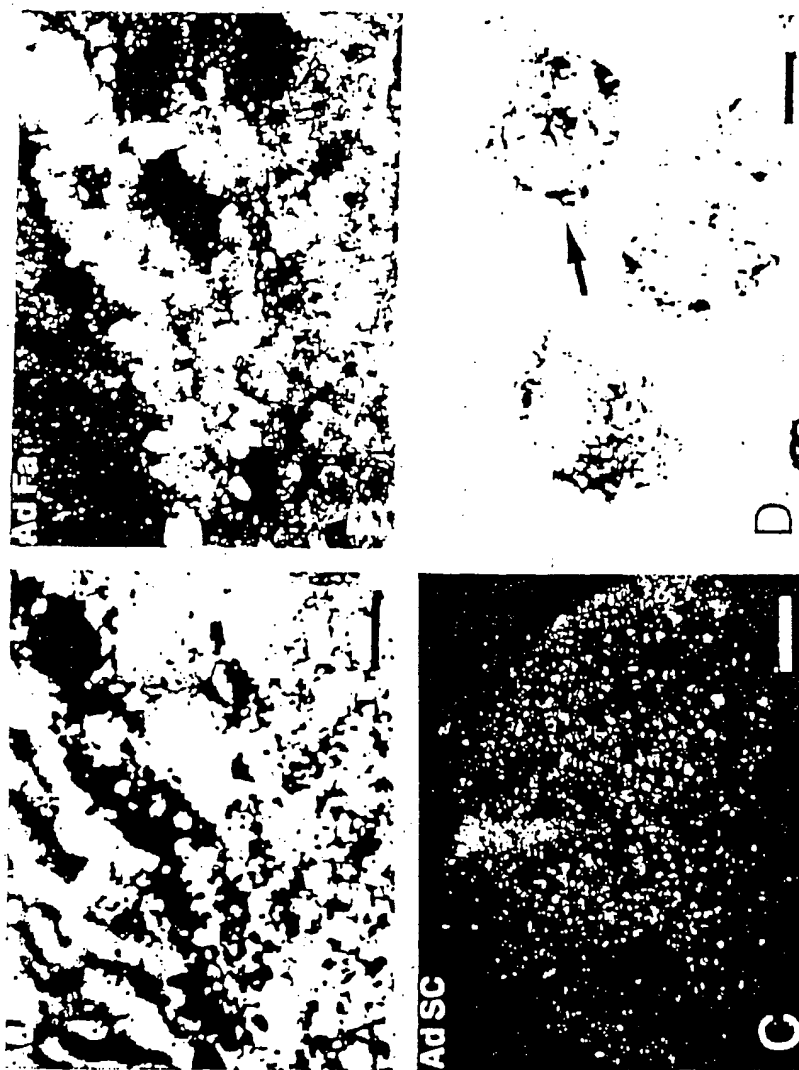


Fig. 15

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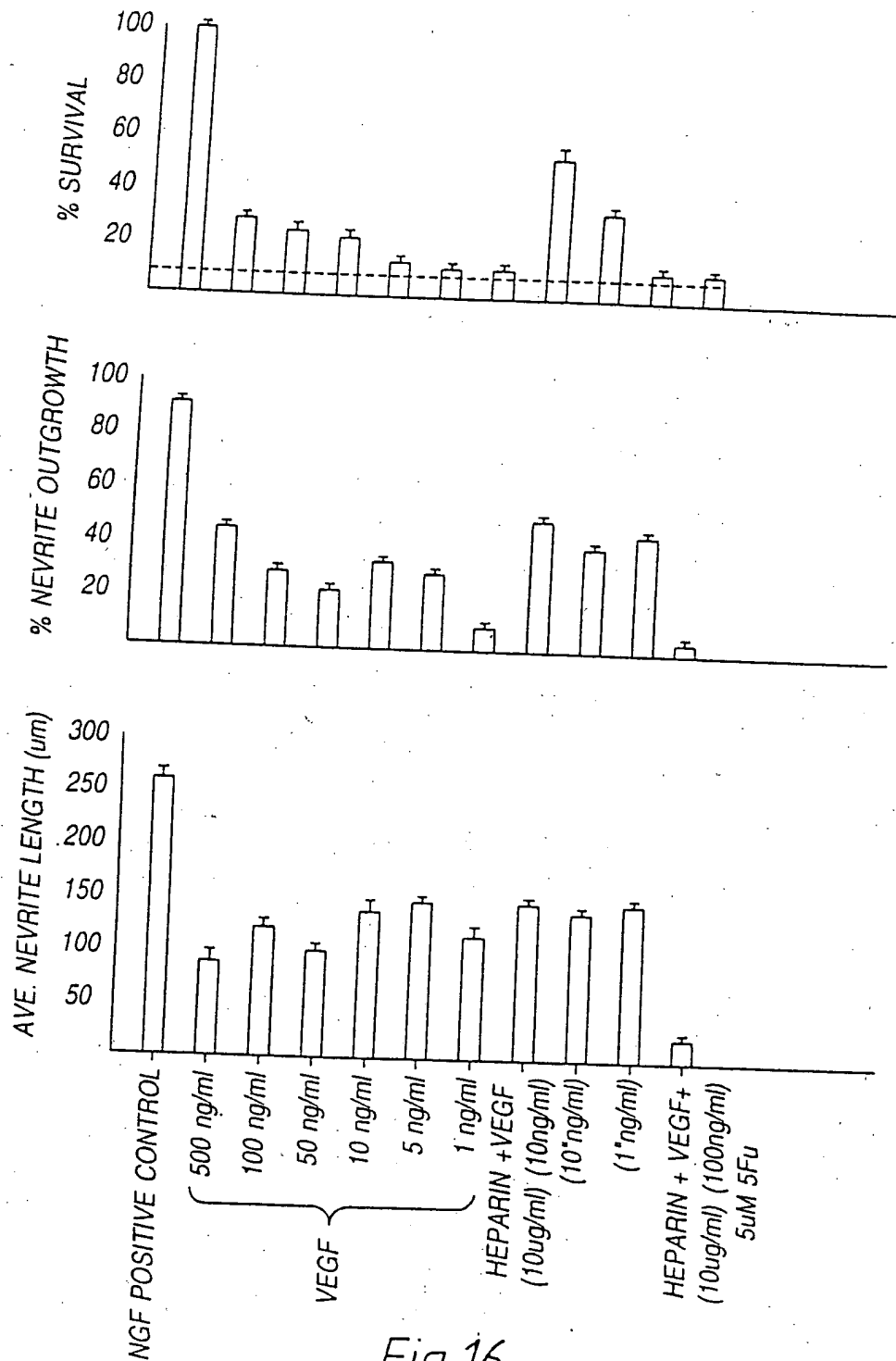
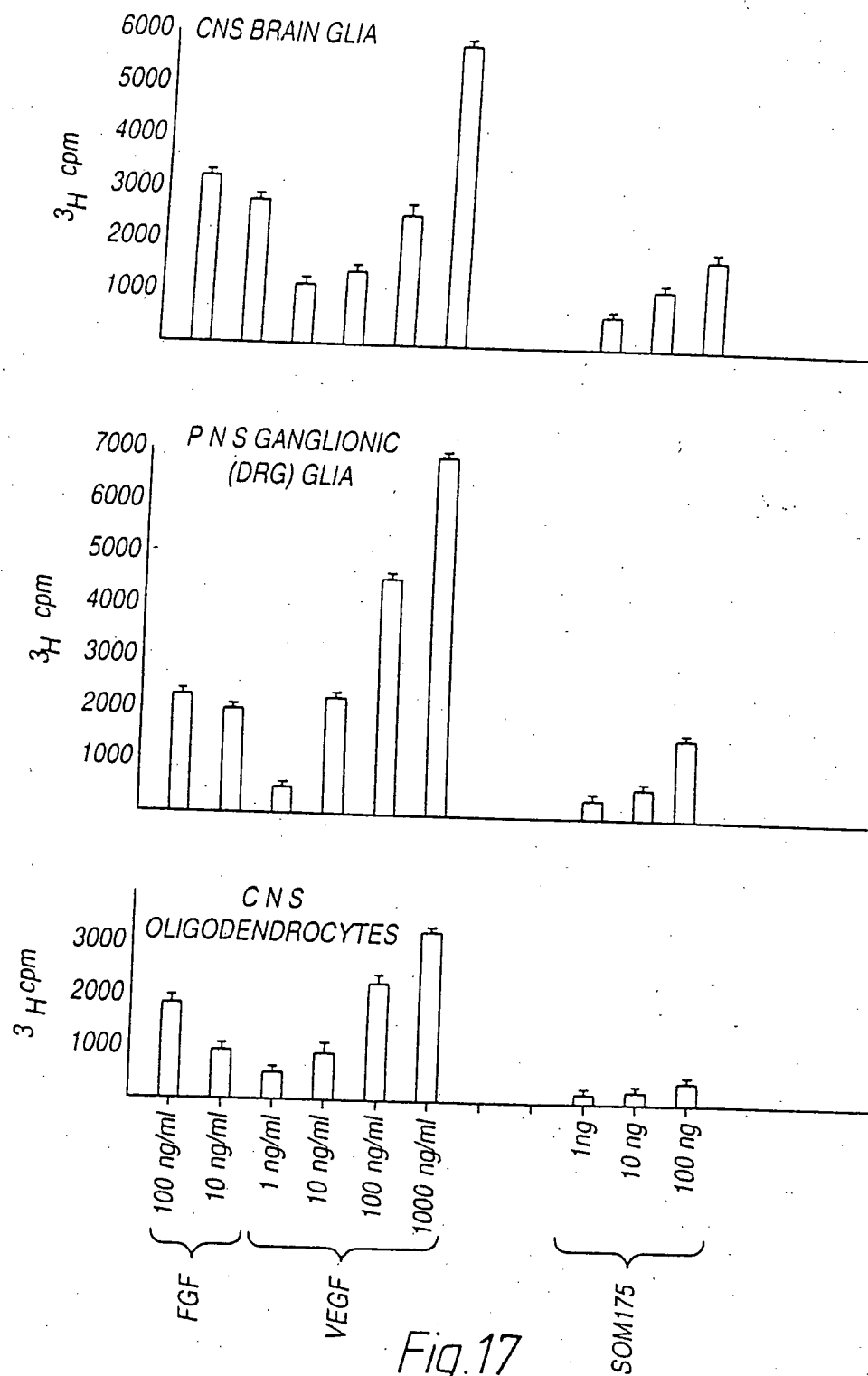


Fig.16

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MOUSE ASTROGLIAL CELLS

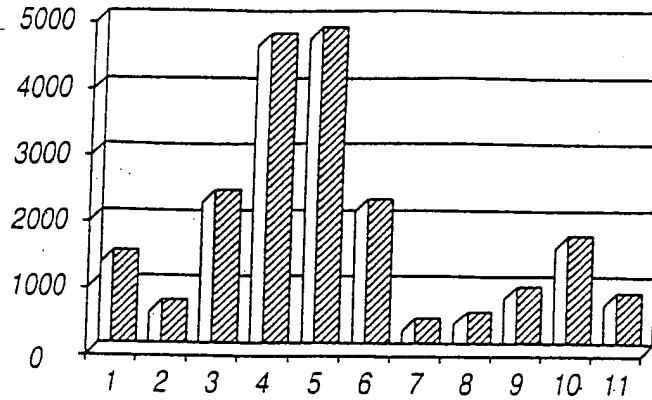


Fig.18

MOUSE OLIGODENDROGLIAL CELLS

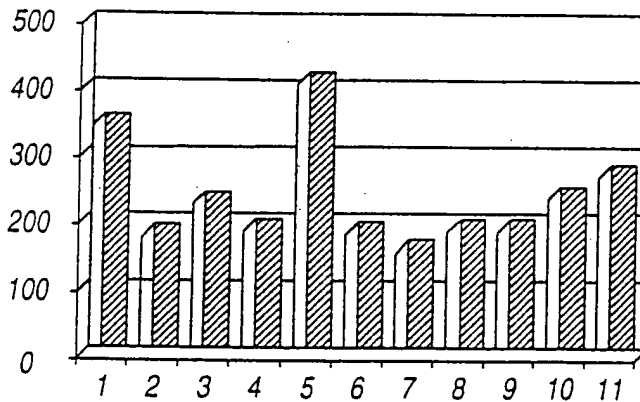


Fig.19

MOUSE FOREBRAIN NEURONS

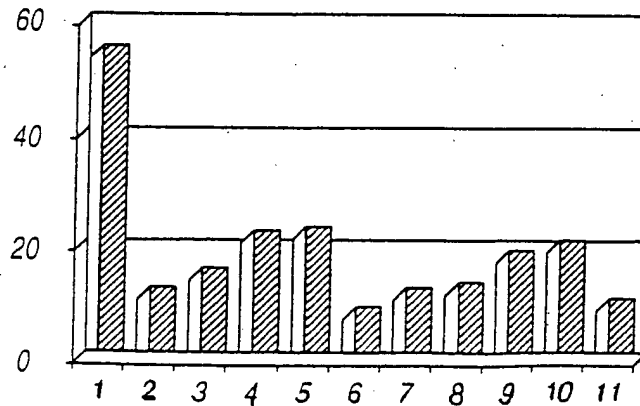


Fig.20